

SCORE Search Results Details for Application 10747994 and Search Result us-10-747-994-2.rag.

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OM protein - protein search, using sw model

Run on: May 30, 2006, 14:37:59 ; Search time 87 Seconds
(without alignments)
1813.100 Million cell updates/sec

Title: US-10-747-994-2
Perfect score: 1804
Sequence: 1 MSFYPCNTTASVRSGNSATV.....PLLYRNWHCHFYTQNVESL 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OM protein - protein search, using sw model

Run on: May 30, 2006, 14:44:59 ; Search time 49 Seconds
(without alignments)
616.287 Million cell updates/sec

Title: US-10-747-994-2
Perfect score: 1804
Sequence: 1 MSFYPCNTTASVRSGNSATV.....PLLYRNWHCHFYTQNVESL 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1342	74.4	359	1	US-08-812-203-3	Sequence 3, Appli

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OM protein - protein search, using sw model

Run on: May 30, 2006, 14:45:44 ; Search time 183 Seconds
(without alignments)
873.274 Million cell updates/sec

Title: US-10-747-994-2
Perfect score: 1804
Sequence: 1 MSFYPCNTTASVRSGNSATV.....PLLYRNWHCHFYTQNVESL 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1804	100.0	345	5	US-10-747-994-2
2	1342	74.4	359	4	US-10-225-567A-287
3	1342	74.4	359	5	US-10-689-861-4

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OM protein - protein search, using sw model

Run on: May 30, 2006, 14:46:39 ; Search time 16 Seconds
(without alignments)
240.149 Million cell updates/sec

Title: US-10-747-994-2
Perfect score: 1804
Sequence: 1 MSFYPCNTTASVRSNGSATV.....PLLYRNWHCHFYTQNVESL 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	540.5	30.0	289	7	US-11-293-697-3907	Sequence 3907, Ap

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OM protein - protein search, using sw model

Run on: May 30, 2006, 14:39:54 ; Search time 40 Seconds
(without alignments)
829.870 Million cell updates/sec

Title: US-10-747-994-2
Perfect score: 1804
Sequence: 1 MSFYPCNTTASVRSGNSATV.....PLLYRNWHCHFYTQNVESL 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1342	74.4	359	2 I39153	prostanoid DP rece
2	911.5	50.5	231	2 I59269	prostaglandin D re
3	711	39.4	362	2 S66674	prostaglandin E re
4	700.5	38.8	358	2 I38920	prostaglandin E2 r
5	697.5	38.7	358	2 S51312	EP2 prostaglandin
6	626.5	34.7	417	2 A54416	prostacyclin recep